Figure 1
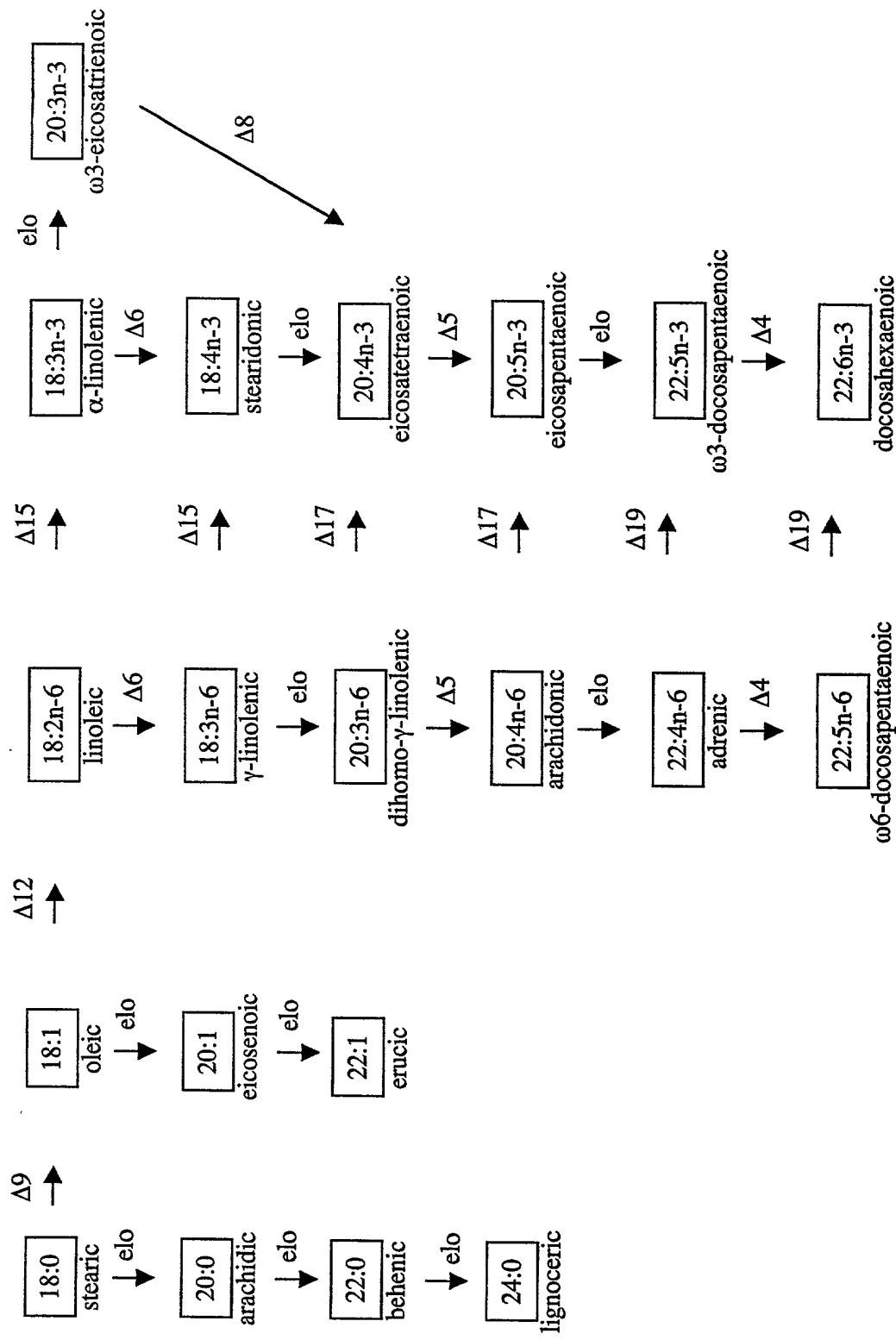## Fatty Acid Biosynthetic Pathway

Figure 2

Gene Sequence of *sdd17*, an Omega-3 Fatty Acid Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

```
   1  ATGACTGAGG ATAAGACGAA GGTCGAGTTC CCGACGCTCA CGGAGCTCAA
  51  GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
 101  ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCGCTGCTC
 151  TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTC TGCTCCACGC
 201  GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
 251  TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC
 301  AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
 351  GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
 401  ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
 451  CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTTGTCTA
 501  CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
 551  ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC
 601  TGGGCCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
 651  TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT
 701  TCCTCGTCAT TACGACCTTC TTGCACCACA CGACGAAGC GACGCCGTGG
 751  TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
 801  CCGCTCGTAC GGCGCGTTCG TGGACAACCT GAGCCACCAC ATTGGCACGC
 851  ACCAGGTCCA CCACTTGTTC CCGATCATTC CGCACTACAA GCTCAACGAA
 901  GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
 951  CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001  ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051  GCGGCCGCCA AGGCCAAGTC GGACTAA
```

Figure 3

Amino Acid Sequence of an Omega-3 Fatty Acid Desaturase (SDD17) from *Saprolegnia diclina* (ATCC 56851)

```
  1   MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL

 51   YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVGHD CGHSAFSRYH

101   SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL

151   QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV

201   WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW

251   YGDSEWTYVK GNLSSVDRSY GAFVDNLSHH IGTHQVHHLF PIIPHYKLNE

301   ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA

351   AAAKAKSD*
```

Figure 4

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep) & *Synechocystis* sp. Delta 15-desaturase (SYCDESB)

```
Frame: 2 initn: 733 init1: 305 opt: 689 Z-score: 996.8 expect(): 1.5e-47
  40.9% identity in 269 aa overlap
  (76-336:204-471)

               50        60        70        80        90        100
SDD17.pep   SAALLYAARSTPFIADNVLLHALVCATYIYVQGVIFWGFFTVGHDCGHSAFSRYHSVNFI
                    :||::||::|:|:||||||||||::||: :::|
SYCDESB     YFFLDVGLIAGFYALAAYLDSWFFYPIFWLIQGTLFWSLFVVGHDCGHGSFSKSKTLNNW
              530       560       590       620       650       680

              110       120       130       140       150       160
SDD17.pep   IGCIMHSAILTPFESWRVTHRHHHKNTGNIDKDEIFYPHRSVKDLQ-----DVRQWVYTLG
            || : |: ||:|:::||::|| || |||||| || :|| | | : |
SYCDESB     IGHLSHTPILVPYHGWRISHRTHHANTGNIDTDESWYPVSEQKYNQMAWYEKLLRFYLPL
              710       740       770       800       830       860

                  170       180       190       200       210       220
SDD17.pep   GAWFVYLKVGYAPRTMSHFDPWDPLLL-RRASAVIVSLGVWAAFFAAYAYLTYSLGFAVM
             |: :||      |   ||| | :||  : :||::| : ||| : ::||:::|: :
SYCDESB     IAYPIYLFRRSPNRQGSHFMPGSPLFRPGEKAAVLTSTFALAAFVGFLGFLTWQFGWLFL
              890       920       950       980       1010      1040

                  230       240       250       260       270       280
SDD17.pep   GLYYYAPLFVFASFLVITTFLHHNDEATPWYGDSEWTYVKGNLSSVDRSYGAFVDNLSHH
             :| || :||: :| ::||||||:::  ||| ::| ::|| ||::||:|| |:: : |
SYCDESB     LKFYVAPYLVFVVWLDLVTFLHHTEDNIPWYRGDDWYFLKGALSTIDRDYG-FINPIHHD
              1070      1100      1130      1160      1190      1220

                  290       300       310       320       330
SDD17.pep   IGTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITAFFKT---AHLFVNYGAV
            |||| :||:| :|||||| :||: :    :  | :|||| |||||: |: | |:
SYCDESB     IGTHVAHHIFSNMPHYKLRRATEAIKPIIGEYYRYSDEPIWQAFFKSYWACHFVPNQGSG
              1250      1280      1310      1340      1370      1400

            340       350
SDD17.pep   PETAQIFTLKESAAAAKAKSD

SYCDESB     VYYQSPSNGGYQKKPXLILIESNQHREGRQYXMVLLPSDRLMRSMEEVKQSHSKRSALNQ
              1430      1460      1490      1520      1550      1580
```

Figure 5

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)
C. elegans Delta 17-desaturase (CELEFAT)

```
Frame: 1 initn: 490 init1: 222 opt: 502 Z-score: 724.0 expect(): 2.3e-32
  31.6% identity in 310 aa overlap
(2-303:49-347)

                                        10        20        30
SDD17.pep                      MTEDKTKVEFPTLTELKHSIPNACFESNLGL
                               | :: ::::||: ::::|| ||| :|
CELFAT    VTGGDVLVDARASLEEKEAPRDVNANTKQATTEEPRIQLPTVDAFRRAIPAHCFERDLVK
            80       110       140       170       200       230


            40        50        60        70        80        90
SDD17.pep SLYYTARAIFNASASAALLYAARSTPFIADNVLLHALVCATYIVQGVIFWGFFTVGHDC
          |: | :: :   |||    : | :   |: ||   ::  ||: :::|:|||||
CELFAT    SIRYLVQDF------AALTILYFALPAFEYFGLFGYLVWNIFM---GVFGFALFVVGHDC
            260       290       320       350       380


            100       110       120       130       140
SDD17.pep GHSAFSRYHSVNFIIGCIMHSAILTPFESWRVTHRHHHKNIGNIDKD---EIFYPHRSVKD
          |::||   :::| :|| |   | :::|: |: :|: ||  |::|||  ::: :: :
CELFAT    LHGSFSDNQNLNDFIGHIAFSPLFSPYFPWQKSHKLHHAFTNHIDKDHGHVWIQDKDWEA
            410       440       470       500       530       560


          150       160       170       180       190       200
SDD17.pep LQDVRQWV-----YTLGGAWF-VYLKVGYAPRIMSHFDPWDPLLLRRASAVIVSLGVWAAF
          : : ::|      ::   || ||   |:    ||| |:: |:: :: |    ::
CELFAT    MPSWKRWFNPIPFSGWLKWFPVYTLFGFC---DGSHFWPYSSLFVRNSDRVQCVISGICCC
            590       620       650       680       710       740


          210       220       230       240       250       260
SDD17.pep FAAYAYLTYSLGFAVMGLYYYAPLFVFASFLVITTFLHHNDEATPWYGDSEWTYVKGNLS
          ||   ||  : :::   ||::||  |: :|||:|:|:| |::: |   :||::|:|: :
CELFAT    VCAYIALTIAGSYSNWFWYYWVPLSFFGLMLVIVTYLQHVDDVAEVYEADEWSFVRGQTQ
            770       800       830       860       890       920


          270       280       290       300       310       320
SDD17.pep SVDRSYGAFVDNLSHHI-GTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITA
          ::|| ||  :|: ||| | |:||: ||||:| |||:
CELFAT    TIDRYYGLGLDTTMHHITDGHVAHHFFNKIPHYHLIEATEGVKKVLEPLSDTQYGYKSQV
            950       980       1010      1040      1070      1100


          330       340       350
SDD17.pep FFKTAHLFVNYGAVPETAQIFTLKESAAAAKAKSD

CELFAT    NYDFFARFLWFNYKLDYLVHKTAGIMQFRTTLEEKAKAKXKNIPCRSRVQQQLLRFHRFC
            1130      1160      1190      1220      1250      1280
```

Figure 6

Gene Sequence of *sdd12*, a Delta 12-Desaturase Gene from *Saprolegnia diclina* (ATCC 56851)

```
   1   ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
  51   GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
 101   CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
 151   CGCAGCGCTG CCACTAGCTT TTACCATTTG GCCAAGAACC TTGCGATCTG
 201   CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
 251   TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG
 301   TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
 351   CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
 401   TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
 451   TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGACGCCGCG
 501   GTCCGTCGTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC
 551   TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
 601   GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
 651   CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCCTCCCA AAGGAGCGCC
 701   TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
 751   GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT
 801   CGTGCCGTAC CTCATTTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
 851   AGCACACGGA TACGTACGTG CCCCACTTCC GCGGCGACGA GTGGAACTGG
 901   CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
 951   CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT
1001   CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCCC
1051   CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT
1101   CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG
1151   TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA
```

Figure 7

Amino Acid Sequence of a Delta 12-Desaturase (SDD12) from *Saprolegnia diclina* (ATCC 56851)

```
  1    MCKGQAPSKA  DVFHAAGYRP  VAGTPEPLPL  EPPTITLKDL  RAAIPAHCFE

 51    RSAATSFYHL  AKNLAICAGV  FAVGLKLAAA  DLPLAAKLVA  WPIYWFVQGT

101    YFTGIWVIAH  ECGHQAFSAS  EILNDTVGII  LHSLLFVPYH  SWKITHRRHH

151    SNTGSCENDE  VFTPTPRSVV  EAKHDHSLLE  ESPLYNLYGI  VMMLLVGWMP

201    GYLFFNATGP  TKYAGLAKSH  FNPYAAFFLP  KERLSIWWSD  LCFLAALYGF

251    GYGVSVFGLL  DVARHYIVPY  LICNAYLVLI  TYLQHTDTYV  PHFRGDEWNW

301    LRGALCTVDR  SFGAWIDSAI  HHIADTHVTH  HIFSKTPFYH  AIEATDAITP

351    LLGKYYLIDP  TPIPLALWRS  FTHCKYVEDD  GNVVFYKRKL  EEK*
```

Figure 8

Comparative analysis of *S. diclina* Delta 12-desaturase (SDD12.pep) & *G. hirsutum* Delta 12-desaturase (GHO6DES)

```
Frame: 3 initn: 992 init1: 413 opt: 1086 Z-score: 1531.8 expect(): 2.3e-77
                   45.6% identity in 379 aa overlap
                        (9-380:14-384)


                          10        20              30        40
SDD12.pep      MCKGQAPSKADVFHAAGYRPVAGTPEP--------LPLEPPTITLKDLRAAIPAHC
               ||: : |:|  |: |  |          :|:| | :|| ::: ||| ||
GHO6DESAT   LRVSSTWRXTAFFKASKMGAGGRMPIDGIKEENRGSVNRVPIEKPPFTLGQIKQAIPPHC
               10        40        70       100       130       160


                   50        60        70        80        90       100
SDD12.pep      FERSAATSFYHLAKNLAICAGVFAVGLKLAAADLPLAAKLVAWPIYWFVQGTYFTGIWVI
               |:||   || ::::: :  :  : :: :      ||   : :|||:|| :|| :||:|||
GHO6DESAT   FRRSLLRSFSYVVHDLCLASFFYYIATSYFHF-LPQPFSYIAWPVYWVLQGCILTGVWVI
               190       220       250       280       310       340


                  110       120       130       140       150       160
SDD12.pep      AHECGHQAFSASEILNDTVGIILHSLLFVPYHSWKITHRRHHSNTGSCENDEVFTPTPRS
               |||  ||:||   : ::||||:||| |:||| ||||:|||||||||| | |||:| |:|
GHO6DESAT   AHEWGHHAFRDYQWVDDTVGLILHSALLVPYFSWKISHRRHHSNTGSMERDEVFVPKPKS
               370       400       430       460       490       520


                  170       180       190       200       210       220
SDD12.pep      VVEAKHDHSLLEESPLYNLYGIVMMLLVGWMPGYLFFNATGPTKYAGLAKSHFNPYAAFF
               :      :   ::|    : ::|:  |  :||  |  |  ||::  :|     ||:|||: ::
GHO6DESAT   KLSC----FAKYLNNPPGRVLSLVVTLTLGW-PMYLAFNVSG--RYYDRLASHYNPYGPIY
                       550       580       610       640       670


                  230       240       250       260       270       280
SDD12.pep      LPKERLSIWWSDLCFLAALYGFGYGVSVFGLLDVARHYIVPYLICNAYLVLITYLQHTDT
               :|||::: ||  ::|::|  :   ::: ||  :     | |  || ||:||||||||||| :
GHO6DESAT   SDRERLQVYISDTGIFAVIYVLYKIAATKGLAWLLCTYGVPLLIVNAFLVLITYLQHTHS
               700       730       760       790       820       850


                  290       300       310       320       330       340
SDD12.pep      YVPHFRGDEWNWLRGALCTVDRSFGAWIDSAIHHIADTHVTHHIFSKTPFYHAIEATDAI
               :||: ::||:||||||| |:||:||: ::::::|:|:||||:||:|    |||:||| ||
GHO6DESAT   ALPHYDSSEWDWLRGALSTMDRDFGV-LNKVFHNITDTHVAHHLFSTMPHYHAMEATKAI
               880       910       940       970      1000      1030


                     350       360       370       380       390
SDD12.pep         TPLLGKYYLIDPTPIPLALWRSFTHCKYVEDDGNVVFYKRKLEEK
                  |:|||||  :| |||  |:||    :| ||| |
GHO6DESAT   KPILGKYYPFDGTPIYKAMWREAKECLYVEPDVGGGGGGSKGVFWYRNKFXRPTNCLIAG
               1060      1090      1120      1150      1180      1210


GHO6DESAT   RRNQRKTYLLDXCXLGKLIINGRKMWNSCLVVLCIKCCINKLYGRKKKK
               1240      1270      1300      1330      1360
```

Figure 9

Sequence ID:

Sequence ID 1
5'-ATC CGC GCC GCC ATC CCC AAG CAC TGC TGG GTC AAG-3'

Sequence ID 2
5'- GCC CTC TTC GTC CTC GGC CAY GAC TGC GGC CAY GGC TCG TTC TCG-3'

Sequence ID 3
5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 4
5'-CCC TAC CAY GGC TGG CGC ATC TCG CAY CGC ACC CAY CAY CAG AAC-3'

Sequence ID 5
5'-GTT CTG RTG RTG GGT CCG RTG CGA GAT GCG CCA GCC RTG GTA GGG-3'

Sequence ID 6
5'- GGC TCG CAC TTC SAC CCC KAC TCG GAC CTC TTC GTC-3'

Sequence ID 7
5'- GAC GAA GAG GTC CGA GTM GGG GTW GAA GTG CGA GCC-3'

Sequence ID 8
5'- GCG CTG GAK GGT GGT GAG GCC GCC GCG GAW GSA CGA CCA-3'

Sequence ID 9
5'- CTG GGG GAA GAG RTG RTG GAT GAC RTG GGT GCC GAT GTC RTG RTG-3'

Sequence ID 10

5'- GGT GGC CTC GAY GAG RTG GTA RTG GGG GAT CTK GGG GAA GAR RTG-3'

Sequence ID 11
5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 12
5'-TAC GCG TAC CTC ACG TAC TCG CTC G-3'

Sequence ID 13
5'-TTC TTG CAC CAC AAC GAC GAA GCG ACG-3'

Sequence ID 14
5'-GGA GTG GAC GTA CGT CAA GGG CAA C-3'

Sequence ID 15
5'-TCA AGG GCA ACC TCT CGA GCG TCG AC-3'

Sequence ID 16
5'-CCC AGT CAC GAC GTT GTA AAA CGA CGG CCA G-3'

Sequence ID 17
 5'- AGC GGA TAA CAA TTT CAC ACA GGA AAC AGC -3'

Sequence ID 18
5'-GGT AAA AGA TCT CGT CCT TGT CGA TGT TGC-3'

Sequence ID 19
5'-GTC AAA GTG GCT CAT CGT GC-3'

Sequence ID 20
5'-CGA GCG AGT ACG TGA GGT ACG CGT AC-3'

Sequence ID 21
5'-TCA ACA GAA TTC ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 22
5'-AAA AGA AAG CTT CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 23
      5'-TCA ACA AAG CTT ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC
      CCG-3'

Sequence ID 24
      5'-AAA AGA GAA TTC CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT
      GGC-3'

Sequence ID 25
      1 ATGACTGAGG ATAAGACGAA GGTCGAGTTC CCGACGCTCA CGGAGCTCAA
     51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
    101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCGCTGCTC
    151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTC TGCTCCACGC
    201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
    251 TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC
    301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
    351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
    401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
    451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTTGTCTA
    501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
    551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC
    601 TGGGCCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
    651 TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT
    701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG
    751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
    801 CCGCTCGTAC GGCGCGTTCG TGGACAACCT GAGCCACCAC ATTGGCACGC
    851 ACCAGGTCCA CCACTTGTTC CCGATCATTC CGCACTACAA GCTCAACGAA
    901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
    951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
   1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA GAGTCGGCC
   1051 GCGGCCGCCA AGGCCAAGTC GGACTAA

Sequence ID 26

```
  1  MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL

 51  YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVGHD CGHSAFSRYH

101  SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL

151  QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV

201  WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW

251  YGDSEWTYVK GNLSSVDRSY GAFVDNLSHH IGTHQVHHLF PIIPHYKLNE

301  ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA

351  AAAKAKSD*
```

Sequence ID 27

```
   1  ATGGCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
  51  GCCGGTGGCC GGCAAGAAGG CCTTTACATG CAGGAGGTC GCGCAGCACA
 101  ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
 151  ACCGAGTGGG CCAACAAGCA CCCCGGCGGC CGCGAGATGG TGCTGCTGCA
 201  CGCCGGTCGC GAGGCCACCG ACACGTTCGA CTCGTACCAC CCGTTCAGCG
 251  ACAAGGCCGA GTCGATCTTG AACAAGTATG AGATTGGCAC GTTCACGGGC
 301  CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
 351  CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
 401  ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTCGCCGGC
 451  CTCGCCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
 501  GGCCGCGGCG CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
 551  TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC
 601  GTCGTCGGCC GCTTTGCCAT GGACTGGTTT GCCGGCGGCT CGATGGTGTC
 651  ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACACG AACGTCGCGG
 701  GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC
 751  GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
 801  TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
 851  CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
 901  GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT
 951  CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001  ACCTTGCGAT CTTCTTCCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG
1051  TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG
1101  CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA
```

```
1151    AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201    GGCGCGCTCA ACTACCAGGT CGTGCACCAC TTGTTCCCCA GCGTGTCGCA
1251    GTACCACTAC CCGGCGATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT
1301    ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC
1351    CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401    CCACATGGGC TAA
```

Sequence ID 28

```
  1    ATGGCAAACA GCAGCGTGTG GGATGATGTG GTGGGCCGCG TGGAGACCGG
 51    CGTGGACCAG TGGATGGATG GCGCCAAGCC GTACGCACTC ACCGATGGGC
101    TCCCGATGAT GGACGTGTCC ACCATGCTGG CATTCGAGGT GGGATACATG
151    GCCATGCTGC TCTTCGGCAT CCCGATCATG AAGCAGATGG AGAAGCCTTT
201    TGAGCTCAAG ACCATCAAGC TCTTGCACAA CTTGTTTCTC TTCGGACTTT
251    CCTTGTACAT GTGCGTGGAG ACCATCCGCC AGGCTATCCT CGGAGGCTAC
301    AAAGTGTTTG AAACGACAT GGAGAAGGGC AACGAGTCTC ATGCTCAGGG
351    CATGTCTCGC ATCGTGTACG TGTTCTGCGT GTCCAAGGCA TACGAGTTCT
401    TGGATACCGC CATCATGATC CTTTGCAAGA AGTTCAACCA GGTTTCCTTC
451    TTGCATGTGT ACCACCATGC CACCATTTTT GCCATCTGGT GGGCTATCGC
501    CAAGTACGCT CCAGGAGGTG ATGCGTACTT TTCAGTGATC CTCAACTCTT
551    TCGTGCACAC CGTCATGTAC GCATACTACT TCTTCTCCTC CCAAGGGTTC
601    GGGTTCGTGA AGCCAATCAA GCCGTACATC ACCACCCTTC AGATGACCCA
651    GTTCATGGCA ATGCTTGTGC AGTCCTTGTA CGACTACCTC TTCCCATGCG
701    ACTACCCACA GGCTCTTGTG CAGCTTCTTG AGTGTACAT GATCACCTTG
751    CTTGCCCTCT TCGGCAACTT TTTTGTGCAG AGCTATCTTA AAAAGCCAAA
801    AAAGAGCAAG ACCAACTAA
```

Sequence ID 29

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  1    MTVGFDETVT MDTVRNHNMP DDAWCAIHGT VYDITKFSKV HPGGDIIMLA
 51    AGKEATILFE TYHIKGVPDA VLRKYKVGKL PQGKKGETSH MPTGLDSASY
101    YSWDSEFYRV LRERVAKKLA EPGLMQRARM ELWAKAIFLL AGFWGSLYAM
151    CVLDPHGGAM VAAVTLGVFA AFVGTCIQHD GSHGAFSKSR FMNKAAGWTL
201    DMIGASAMTW EMQHVLGHHP YTNLIEMENG LAKVKGADVD PKKVDQESDP
251    DVFSTYPMLR LHPWHRQRFY HKFQHLYAPL IFGFMTINKV ISQDVGVVLR
301    KRLFQIDANC RYGSPWNVAR FWIMKLLTTL YMVALPMYMQ GPAQGLKLFF
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351 MAHFTCGEVL ATMFIVNHII EGVSYASKDA VKGVMAPPRT VHGVTPMQVT

401 QKALSAAEST KSDADKTTMI PLNDWAAVQC QTSVNWAVGS WFWNHFSGGL

451 NHQIEHHCFP QNPHTVNVYI SGIVKETCEE YGVPYQAEIS LFSAYFKMLS

501 HLRTLGNEDL TAWST*

Sequence ID 30

    5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC
    CAC TGC TTC -3'

Sequence ID 31

    5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR
    CGG CAT-3'

Sequence ID 32

    5'-CCS STC TAC TGG GCC TGC CAG GGT RTC GTC CTC ACS GGT GTC
    TGG-3'

Sequence ID 33

    5'-CCS STC TAC TGG ATC RYS CAG GGT RTC GTC KGY ACS GGT GTC
    TGG-3'

Sequence ID 34

    5'-GGC GTG GTA GTG CGG CAT SMM CGA GAA GAR GTG GTG GGC GAC
    GTG-3'

Sequence ID 35

    5'-CAC GTA CCT CCA GCA CAC GGA CAC CTA CG-3'

Sequence ID 36

    5'- GAT CGA CAG CGC GAT CCA CCA CAT TGC-3'

Sequence ID 37

    5'- CAA ATG GTA AAA GCT AGT GGC AGC GCT GC-3'

Sequence ID 38

    5'-AGT ACG TGC CCT GGA CGA ACC AGT AGA TG-3'

Sequence ID 39

    5'- TCA ACA GAA TTC ATG TGC AAA GGT CAA GCT CCT TCC AAG GCC
    GAC GTG -3'

Sequence ID 40

    5'- AAA AGA AAG CTT TTA CTT TTC CTC GAG CTT GCG CTT GTA AAA
    CAC AAC-3'

Sequence ID 41

```
   1  ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
  51  GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
 101  CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
 151  CGCAGCGCTG CCACTAGCTT TTACCATTTG GCCAAGAACC TTGCGATCTG
 201  CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
 251  TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG
 301  TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
 351  CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
 401  TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
 451  TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGACGCCGCG
 501  GTCCGTCGTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC
 551  TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
 601  GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
 651  CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCCTCCCA AAGGAGCGCC
 701  TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
 751  GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT
 801  CGTGCCGTAC CTCATTTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
 851  AGCACACGGA TACGTACGTG CCCCACTTCC GCGGCGACGA GTGGAACTGG
 901  CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
 951  CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT
1001  CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCCC
1051  CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT
1101  CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG
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1151   TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Sequence ID 42

    1   MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE

   51   RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWFVQGT

  101   YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH

  151   SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP

  201   GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSD LCFLAALYGF

  251   GYGVSVFGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW

  301   LRGALCTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP

  351   LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*